



## SEQUENCE LISTING

RECEIVED  
OCT 12 2001  
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## (1) GENERAL INFORMATION:

(i) APPLICANT: Pastan, Ira  
Chang, Kai

(ii) TITLE OF INVENTION: Mesothelin, a Differentiation Antigen  
Present on Mesothelium, Mesotheliomas and Ovarian Cancers  
and Methods and Kits for Targeting the Antigen

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Townsend and Townsend and Crew LLP  
(B) STREET: Two Embarcadero Center, Eighth Floor  
(C) CITY: San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94111-3834

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: Not yet assigned  
(B) FILING DATE: Not yet assigned  
(C) CLASSIFICATION:  
*B 84*

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/776,271  
(B) FILING DATE: 01-DEC-1998

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: WO PCT/US97/00224  
(B) FILING DATE: 03-JAN-1997

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 60/010,166  
(B) FILING DATE: 05-JAN-1996

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Faris, Susan K.  
(B) REGISTRATION NUMBER: 41,739  
(C) REFERENCE/DOCKET NUMBER: 015280-259110US

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (415) 576-0200  
(B) TELEFAX: (415) 576-0300

## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 100..1986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGGAATTCCG GTGGCCGGCC ACTCCCGTCT GCTGTGACGC GCGGACAGAG AGCTACCGGT	60
GGACCCACGG TGCCTCCCTC CCTGGGATCT ACACAGACC ATG GCC TTG CAA CGG Met Ala Leu Gln Arg	114
1 5	
CTC GAC CCC TGT TGG TCC TGT GGG GAC CGC CCT GGC AGC CTC CTG TTC Leu Asp Pro Cys Trp Ser Cys Gly Asp Arg Pro Gly Ser Leu Leu Phe	162
10 15 20	
CTG CTC TTC AGC CTC GGA TGG GTG CAT CCC GCG AGG ACC CTG GCT GGA Leu Leu Phe Ser Leu Gly Trp Val His Pro Ala Arg Thr Leu Ala Gly	210
25 30 35	
GAG ACA GGG ACG GAG TCT GCC CCC CTG GGG GGA GTC CTG ACA ACC CCC Glu Thr Gly Thr Glu Ser Ala Pro Leu Gly Gly Val Leu Thr Thr Pro	258
40 45 50	
<i>B7</i>	
CAT AAC ATT TCC AGC CTC TCC CCT CGC CAA CTC CTT GGC TTC CCG TGT His Asn Ile Ser Ser Leu Ser Pro Arg Gln Leu Leu Gly Phe Pro Cys	306
55 60 65	
GCG GAG GTG TCC GGC CTG AGC ACG GAG CGT GTC CGG GAG CTG GCT GTG Ala Glu Val Ser Gly Leu Ser Thr Glu Arg Val Arg Glu Leu Ala Val	354
70 75 80 85	
GCC TTG GCA CAG AAG AAT GTC AAG CTC TCA ACA GAG CAG CTG CGC TGT Ala Leu Ala Gln Lys Asn Val Lys Leu Ser Thr Glu Gln Leu Arg Cys	402
90 95 100	
CTG GCT CAC CGG CTC TCT GAG CCC CCC GAG GAC CTG GAC GCC CTC CCA Leu Ala His Arg Leu Ser Glu Pro Pro Glu Asp Leu Asp Ala Leu Pro	450
105 110 115	
TTG GAC CTG CTG CTA TTC CTC AAC CCA GAT GCG TTC TCG GGG CCC CAG Leu Asp Leu Leu Leu Phe Leu Asn Pro Asp Ala Phe Ser Gly Pro Gln	498
120 125 130	
GCC TGC ACC CGT TTC TTC TCC CGC ATC ACG AAG GCC AAT GTG GAC CTG Ala Cys Thr Arg Phe Phe Ser Arg Ile Thr Lys Ala Asn Val Asp Leu	546
135 140 145	

CTC CCG AGG GGG GCT CCC GAG CGA CAG CGG CTG CTG CCT GCG GCT CTG Leu Pro Arg Gly Ala Pro Glu Arg Gln Arg Leu Leu Pro Ala Ala Leu 150 155 160 165	594
GCC TGC TGG GGT GTG CGG GGG TCT CTG CTG AGC GAG GCT GAT GTG CGG Ala Cys Trp Gly Val Arg Gly Ser Leu Leu Ser Glu Ala Asp Val Arg 170 175 180	642
GCT CTG GGA GGC CTG GCT TGC GAC CTG CCT GGG CGC TTT GTG GCC GAG Ala Leu Gly Gly Leu Ala Cys Asp Leu Pro Gly Arg Phe Val Ala Glu 185 190 195	690
TCG GCC GAA GTG CTG CTA CCC CGG CTG GTG AGC TGC CCG GGA CCC CTG Ser Ala Glu Val Leu Leu Pro Arg Leu Val Ser Cys Pro Gly Pro Leu 200 205 210	738
GAC CAG GAC CAG CAG GAG GCA GCC AGG GCG GCT CTG CAG GGC GGG GGA Asp Gln Asp Gln Gln Glu Ala Ala Arg Ala Ala Leu Gln Gly Gly Gly 215 220 225	786
CCC CCC TAC GGC CCC CCG TCG ACA TGG TCT GTC TCC ACG ATG GAC GCT Pro Pro Tyr Gly Pro Pro Ser Thr Trp Ser Val Ser Thr Met Asp Ala 230 235 240 245	834
CTG CGG GGC CTG CTG CCC GTG CTG GGC CAG CCC ATC ATC CGC AGC ATC Leu Arg Gly Leu Leu Pro Val Leu Gly Gln Pro Ile Ile Arg Ser Ile 250 255 260	882
CCG CAG GGC ATC GTG GCC GCG TGG CGG CAA CGC TCC TCT CGG GAC CCA Pro Gln Gly Ile Val Ala Ala Trp Arg Gln Arg Ser Ser Arg Asp Pro 265 270 275	930
TCC TGG CGG CAG CCT GAA CGG ACC ATC CTC CGG CCG CGG TTC CGG CGG Ser Trp Arg Gln Pro Glu Arg Thr Ile Leu Arg Pro Arg Phe Arg Arg 280 285 290	978
GAA GTG GAG AAG ACA GCC TGT CCT TCA GGC AAG AAG GGC CGC GAG ATA Glu Val Glu Lys Thr Ala Cys Pro Ser Gly Lys Lys Ala Arg Glu Ile 295 300 305	1026
GAC GAG AGC CTC ATC TTC TAC AAG AAG TGG GAG CTG GAA GCC TGC GTG Asp Glu Ser Leu Ile Phe Tyr Lys Lys Trp Glu Leu Glu Ala Cys Val 310 315 320 325	1074
GAT GCG GCC CTG CTG GCC ACC CAG ATG GAC CGC GTG AAC GCC ATC CCC Asp Ala Ala Leu Leu Ala Thr Gln Met Asp Arg Val Asn Ala Ile Pro 330 335 340	1122
TTC ACC TAC GAG CAG CTG GAC GTC CTA AAG CAT AAA CTG GAT GAG CTC Phe Thr Tyr Glu Gln Leu Asp Val Leu Lys His Lys Leu Asp Glu Leu 345 350 355	1170
TAC CCA CAA GGT TAC CCC GAG TCT GTG ATC CAG CAC CTG GGC TAC CTC Tyr Pro Gln Gly Tyr Pro Glu Ser Val Ile Gln His Leu Gly Tyr Leu 360 365 370	1218
TTC CTC AAG ATG AGC CCT GAG GAC ATT CGC AAG TGG AAT GTG ACG TCC Phe Leu Lys Met Ser Pro Glu Asp Ile Arg Lys Trp Asn Val Thr Ser 375 380 385	1266

CTG GAG ACC CTG AAG GCT TTG CTT GAA GTC GAC AAA GGG CAC GAA ATG 1314  
 Leu Glu Thr Leu Lys Ala Leu Leu Glu Val Asp Lys Gly His Glu Met  
 390 395 400 405

AGT CCT CAG GCT CCT CGG CGG CCC CTC CCA CAG GTG GCC ACC CTG ATC 1362  
 Ser Pro Gln Ala Pro Arg Arg Pro Leu Pro Gln Val Ala Thr Leu Ile  
 410 415 420

GAC CGC TTT GTG AAG GGA AGG GGC CAG CTA GAC AAA GAC ACC CTA GAC 1410  
 Asp Arg Phe Val Lys Gly Arg Gly Gln Leu Asp Lys Asp Thr Leu Asp  
 425 430 435

ACC CTG ACC GCC TTC TAC CCT GGG TAC CTG TGC TCC CTC AGC CCC GAG 1458  
 Thr Leu Thr Ala Phe Tyr Pro Gly Tyr Leu Cys Ser Leu Ser Pro Glu  
 440 445 450

GAG CTG AGC TCC GTG CCC CCC AGC ATC TGG GCG GTC AGG CCC CAG 1506  
 Glu Leu Ser Ser Val Pro Pro Ser Ser Ile Trp Ala Val Arg Pro Gln  
 455 460 465

GAC CTG GAC ACG TGT GAC CCA AGG CAG CTG GAC GTC CTC TAT CCC AAG 1554  
 Asp Leu Asp Thr Cys Asp Pro Arg Gln Leu Asp Val Leu Tyr Pro Lys  
 470 475 480 485

GCC CGC CTT GCT TTC CAG AAC ATG AAC GGG TCC GAA TAC TTC GTG AAG 1602  
 Ala Arg Leu Ala Phe Gln Asn Met Asn Gly Ser Glu Tyr Phe Val Lys  
 490 495 500

ATC CAG TCC TTC CTG GGT GGG GCC CCC ACG GAG GAT TTG AAG GCG CTC 1650  
 Ile Gln Ser Phe Leu Gly Ala Pro Thr Glu Asp Leu Lys Ala Leu  
 505 510 515

AGT CAG CAG AAT GTG AGC ATG GAC TTG GCC ACG GAG GAT TTG AAG GCG CTC 1698  
 Ser Gln Gln Asn Val Ser Met Asp Leu Ala Thr Phe Met Lys Leu Arg  
 520 525 530

ACG GAT GCG GTG CTG CCG TTG ACT GTG GCT GAG GTG CAG AAA CTT CTG 1746  
 Thr Asp Ala Val Leu Pro Leu Thr Val Ala Glu Val Gln Lys Leu Leu  
 535 540 545

GGA CCC CAC GTG GAG GGC CTG AAG GCG GAG GAG CGG CAC CGC CCG GTG 1794  
 Gly Pro His Val Glu Gly Leu Lys Ala Glu Glu Arg His Arg Pro Val  
 550 555 560 565

CGG GAC TGG ATC CTA CGG CAG CGG CAG GAC GAC CTG GAC ACG CTG GGG 1842  
 Arg Asp Trp Ile Leu Arg Gln Arg Gln Asp Asp Leu Asp Thr Leu Gly  
 570 575 580

CTG GGG CTA CAG GGC GGC ATC CCC AAC GGC TAC CTG GTC CTA GAC CTC 1890  
 Leu Gly Leu Gln Gly Ile Pro Asn Gly Tyr Leu Val Leu Asp Leu  
 585 590 595

AGC GTG CAA GAG ACC CTC TCG GGG ACG CCC TGC CTC CTA GGA CCT GGA 1938  
 Ser Val Gln Glu Thr Leu Ser Gly Thr Pro Cys Leu Leu Gly Pro Gly  
 600 605 610

CCT GTT CTC ACC GTC CTG GCA CTG CTC CTA GCC TCC ACC CTG GCC 1983  
 Pro Val Leu Thr Val Leu Ala Leu Leu Ala Ser Thr Leu Ala  
 615 620 625

TGAGGGCCCC ACTCCCTTGC TGGCCCCAGC CCTGCTGGGG ATCCCCGCCT GGCCAGGAGC 2043

AGGCACGGGT GATCCCCGTT CCACCCCAAG AGAACTCGCG CTCAGTAAAC GGGAACATGC	2103
CCCCTGCAGA CAAAAAAA AAAAAAAA AAAAA	2138

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Leu Gln Arg Leu Asp Pro Cys Trp Ser Cys Gly Asp Arg Pro			
1	5	10	15
Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val His Pro Ala			
20	25	30	
Arg Thr Leu Ala Gly Glu Thr Gly Thr Glu Ser Ala Pro Leu Gly Gly			
35	40	45	
Val Leu Thr Thr Pro His Asn Ile Ser Ser Leu Ser Pro Arg Gln Leu			
50	55	60	
Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu Arg Val			
65	70	75	80
Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu Ser Thr			
85	90	95	
Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro Glu Asp			
100	105	110	
Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro Asp Ala			
115	120	125	
Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile Thr Lys			
130	135	140	
Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln Arg Leu			
145	150	155	160
Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu Leu Ser			
165	170	175	
Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu Pro Gly			
180	185	190	
Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu Val Ser			
195	200	205	
Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg Ala Ala			
210	215	220	
Leu Gln Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp Ser Val			
225	230	235	240

Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly Gln Pro  
 245 250 255  
 Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg Gln Arg  
 260 265 270  
 Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile Leu Arg  
 275 280 285  
 Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser Gly Lys  
 290 295 300  
 Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys Trp Glu  
 305 310 315 320  
 Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met Asp Arg  
 325 330 335  
 Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu Lys His  
 340 345 350  
 Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val Ile Gln  
 355 360 365  
 His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile Arg Lys  
 370 375 380  
 Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu Val Asp  
 385 390 395 400  
 Lys Gly His Glu Met Ser Pro Gln Ala Pro Arg Arg Pro Leu Pro Gln  
 405 410 415  
 Val Ala Thr Leu Ile Asp Arg Phe Val Lys Gly Arg Gly Gln Leu Asp  
 420 425 430  
 Lys Asp Thr Leu Asp Thr Leu Thr Ala Phe Tyr Pro Gly Tyr Leu Cys  
 435 440 445  
 Ser Leu Ser Pro Glu Glu Leu Ser Ser Val Pro Pro Ser Ser Ile Trp  
 450 455 460  
 Ala Val Arg Pro Gln Asp Leu Asp Thr Cys Asp Pro Arg Gln Leu Asp  
 465 470 475 480  
 Val Leu Tyr Pro Lys Ala Arg Leu Ala Phe Gln Asn Met Asn Gly Ser  
 485 490 495  
 Glu Tyr Phe Val Lys Ile Gln Ser Phe Leu Gly Gly Ala Pro Thr Glu  
 500 505 510  
 Asp Leu Lys Ala Leu Ser Gln Gln Asn Val Ser Met Asp Leu Ala Thr  
 515 520 525  
 Phe Met Lys Leu Arg Thr Asp Ala Val Leu Pro Leu Thr Val Ala Glu  
 530 535 540  
 Val Gln Lys Leu Leu Gly Pro His Val Glu Gly Leu Lys Ala Glu Glu  
 545 550 555 560

Arg His Arg Pro Val Arg Asp Trp Ile Leu Arg Gln Arg Gln Asp Asp  
565 570 575

Leu Asp Thr Leu Gly Leu Gly Leu Gln Gly Gly Ile Pro Asn Gly Tyr  
580 585 590

Leu Val Leu Asp Leu Ser Val Gln Glu Thr Leu Ser Gly Thr Pro Cys  
595 600 605

Leu Leu Gly Pro Gly Pro Val Leu Thr Val Leu Ala Leu Leu Leu Ala  
610 615 620

Ser Thr Leu Ala  
625

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Gly Gly Gly Ser  
1 5

*B7*  
(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Glu Asp Leu Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Glu Asp Leu  
1

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Asp Glu Leu  
1

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Lys Asp Glu Leu  
1

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Pro Arg Phe Arg Arg  
1 5